

16	1292	37.5	2192	2	Q49L15_AEDAE	Q49L15 aedes aegyp
17	1284	37.3	2249	1	DCR1_DROME	Q9vku9 drosophila
18	1283	37.2	2280	2	Q29AU1_DROPS	Q29au1 drosophila
19	1151	33.4	1845	1	DCR1_CAEL	P34529 caenorhabdi
20	1106.5	32.1	1863	2	Q60MW6_CAEBR	Q60mw6 caenorhabdi
21	902	26.2	2043	2	Q27IU2_DROME	Q27iu2 drosophila
22	896	26.0	2043	2	Q27IT7_DROSI	Q27it7 drosophila
23	894	25.9	2043	2	Q27IT4_DROSI	Q27it4 drosophila
24	894	25.9	2043	2	Q27IT9_DROSI	Q27it9 drosophila
25	894	25.9	2043	2	Q27IT6_DROSI	Q27it6 drosophila
26	894	25.9	2043	2	Q27IT8_DROSI	Q27it8 drosophila
27	894	25.9	2043	2	Q27IU7_DROME	Q27iu7 drosophila
28	894	25.9	2043	2	Q27IU0_DROME	Q27iu0 drosophila
29	894	25.9	2043	2	Q27IU5_DROME	Q27iu5 drosophila
30	894	25.9	2043	2	Q27IU9_DROME	Q27iu9 drosophila
31	894	25.9	2043	2	Q27IU4_DROME	Q27iu4 drosophila
32	894	25.9	2043	2	Q27IU8_DROME	Q27iu8 drosophila
33	893	25.9	2043	2	Q27IU3_DROME	Q27iu3 drosophila
34	893	25.9	2043	2	Q27IT5_DROSI	Q27it5 drosophila
35	892	25.9	2043	2	Q27IU6_DROME	Q27iu6 drosophila
36	888	25.8	2043	2	Q27IU1_DROSI	Q27iu1 drosophila
37	713	20.7	149	2	Q862N0_BOVIN	Q862n0 bos taurus
38	631	18.3	1658	2	Q174T8_AEDAE	Q174t8 aedes aegyp
39	624	18.1	1715	2	Q29IA3_DROPS	Q29ia3 drosophila
40	623	18.1	1658	2	Q49L14_AEDAE	Q49L14 aedes aegyp
41	616.5	17.9	1719	2	Q2Q3U0_DROYA	Q2q3u0 drosophila
42	616.5	17.9	1719	2	Q2Q3U4_DROYA	Q2q3u4 drosophila
43	612	17.8	1719	2	Q2Q3U1_DROYA	Q2q3u1 drosophila
44	612	17.8	1719	2	Q2Q3U5_DROYA	Q2q3u5 drosophila
45	612	17.8	1719	2	Q2Q3U3_DROYA	Q2q3u3 drosophila

ALIGNMENTS

RESULT 1

DICER_HUMAN

ID DICER_HUMAN Reviewed; 1912 AA.

AC Q9UPY3; O95943; Q9UQ02;

DT 25-OCT-2002, integrated into UniProtKB/Swiss-Prot.

DT 25-OCT-2002, sequence version 2.

DT 24-JUL-2007, entry version 61.

DE Endoribonuclease Dicer (EC 3.1.26.-) (Helicase with RNase motif)

DE (Helicase-MOI).

GN Name=DICER1; Synonyms=DICER, HERNA, KIAA0928;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=20246304; PubMed=10786632; DOI=10.1016/S0167-4781(99)00221-3;

RA Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,

RA Hamaguchi M.;

RT "Molecular cloning and characterization of a novel human gene (HERNA)

RT which encodes a putative RNA-helicase.";

RL Biochim. Biophys. Acta 1490:163-169(2000).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Lung;

RA Provost P., Dishart D., Doucet D., Hermansson A., Frendewey D.,

RA Samuelsson B., Radmark O.;

RT "RNA binding and processing by recombinant human Dicer.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Brain;

RX MEDLINE=99246063; PubMed=10231032; DOI=10.1093/dnares/6.1.63;

RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,

RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XIII.

RT The complete sequences of 100 new cDNA clones from brain which code

RT for large proteins in vitro.";

RL DNA Res. 6:63-70(1999).

RN [4]

RP SEQUENCE REVISION.

RX MEDLINE=22158633; PubMed=12168954; DOI=10.1093/dnares/9.3.99;

RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;

RT "Construction of expression-ready cDNA clones for KIAA genes: manual

RT curation of 330 KIAA cDNA clones.";

RL DNA Res. 9:99-106(2002).

RN [5]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 1238-1912.

RC TISSUE=Lung;

RX MEDLINE=99162526; PubMed=10051563; DOI=10.1073/pnas.96.5.1881;

RA Provost P., Samuelsson B., Radmark O.;

RT "Interaction of 5-lipoxygenase with cellular proteins.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:1881-1885(1999).

RN [6]

RP INTERACTION WITH PIWIL1.

RX PubMed=14749716; DOI=10.1038/sj.embor.7400070;

RA Tahbaz N., Kolb F.A., Zhang H., Jaronczyk K., Filipowicz W.,

RA Hobman T.C.;

RT "Characterization of the interactions between mammalian PAZ PIWI

RT domain proteins and Dicer.";

RL EMBO Rep. 5:189-194(2004).

RN [7]

RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-654, AND MASS

RP SPECTROMETRY.

RX PubMed=15592455; DOI=10.1038/nbt1046;

RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,

RA Zha X.-M., Polakiewicz R.D., Comb M.J.;

RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer

RT cells.";

RL Nat. Biotechnol. 23:94-101(2005).

CC -!- FUNCTION: Involved in cleaving double-stranded RNA in the RNA

CC interference (RNAi) pathway. It produces 21 to 23 bp dsRNAs

CC (siRNAs) which target the selective destruction of homologous

CC RNAs.

CC -!- SUBUNIT: Interacts with PIWIL1.

CC -!- INTERACTION:

CC Q9UL18:EIF2C1; NbExp=2; IntAct=EBI-395506, EBI-527363;

CC Q9UKV8:EIF2C2; NbExp=1; IntAct=EBI-395506, EBI-528269;

CC Q8CJG0:EIF2C2 (xeno); NbExp=2; IntAct=EBI-395506, EBI-528299;
 CC Q8TBY5:PIWIL1; NbExp=1; IntAct=EBI-395506, EBI-527417;
 CC Q15633:TARBP2; NbExp=4; IntAct=EBI-395506, EBI-978581;
 CC -!- SIMILARITY: Belongs to the helicase family.
 CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
 CC -!- SIMILARITY: Contains 1 helicase ATP-binding domain.
 CC -!- SIMILARITY: Contains 1 helicase C-terminal domain.
 CC -!- SIMILARITY: Contains 1 PAZ domain.
 CC -!- SIMILARITY: Contains 2 RNase III domains.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB028449; BAA78691.1; ALT_INIT; mRNA.
 DR EMBL; AJ132261; CAB38857.2; -; mRNA.
 DR EMBL; AB023145; BAA76772.2; ALT_INIT; mRNA.
 DR UniGene; Hs.87889; -.
 DR HSSP; O67082; 1UF2.
 DR IntAct; Q9UPY3; -.
 DR Ensembl; ENSG00000100697; Homo sapiens.
 DR KEGG; hsa:23405; -.
 DR HGNC; HGNC:17098; DICER1.
 DR HPA; HPA000694; -.
 DR MIM; 606241; gene.
 DR PharmGKB; PA38437; -.
 DR ArrayExpress; Q9UPY3; -.
 DR GermOnline; ENSG00000100697; Homo sapiens.
 DR GO; GO:0005622; C:intracellular; NAS:UniProtKB.
 DR GO; GO:0003725; F:double-stranded RNA binding; IDA:UniProtKB.
 DR GO; GO:0005515; F:protein binding; IPI:IntAct.
 DR GO; GO:0004525; F:ribonuclease III activity; IDA:UniProtKB.
 DR GO; GO:0030423; P:RNA interference, targeting of mRNA for des. . .;
 IEP:UniProtKB.
 DR InterPro; IPR014001; DEAD-like_N.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001159; Ds_RNA_bd.
 DR InterPro; IPR005034; DUF283.
 DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR003100; PAZ.
 DR InterPro; IPR000999; RNase_III.
 DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00035; dsrm; 1.
 DR Pfam; PF03368; DUF283; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF02170; PAZ; 1.
 DR Pfam; PF00636; Ribonuclease_3; 2.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00358; DSRM; 1.
 DR SMART; SM00490; HELICc; 1.
 DR SMART; SM00535; RIBOC; 2.
 DR PROSITE; PS50137; DS_RBD; 1.
 DR PROSITE; PS51192; HELICASE_ATP_BIND_1; 1.
 DR PROSITE; PS51194; HELICASE_CTER; 1.
 DR PROSITE; PS50821; PAZ; 1.
 DR PROSITE; PS00517; RNASE_3_1; 1.

DR PROSITE; PS50142; RNASE_3_2; 2.
 PE 1: Evidence at protein level;
 KW ATP-binding; Endonuclease; Helicase; Hydrolase; Nuclease;
 KW Nucleotide-binding; Phosphorylation; Repeat; RNA-binding;
 KW RNA-mediated gene silencing.
 FT CHAIN 1 1912 Endoribonuclease Dicer.
 FT /FTId=PRO_0000180470.
 FT DOMAIN 41 217 Helicase ATP-binding.
 FT DOMAIN 423 592 Helicase C-terminal.
 FT DOMAIN 881 1032 PAZ.
 FT DOMAIN 1266 1393 RNase III 1.
 FT DOMAIN 1656 1814 RNase III 2.
 FT DOMAIN 1839 1904 DRBM.
 FT NP_BIND 34 41 ATP (Potential).
 FT MOTIF 165 168 DECH box.
 FT MOD_RES 654 654 Phosphotyrosine.
 FT CONFLICT 65 80 VLLTKELSYQIRGDFS -> STLLKSCLYLDLGETSA
 FT (in Ref. 1).
 FT CONFLICT 179 179 I -> F (in Ref. 1).
 FT CONFLICT 185 185 N -> I (in Ref. 1).
 FT CONFLICT 204 204 C -> W (in Ref. 1).
 FT CONFLICT 208 208 E -> D (in Ref. 1).
 FT CONFLICT 213 213 I -> F (in Ref. 1).
 FT CONFLICT 383 384 QQ -> HS (in Ref. 1).
 FT CONFLICT 482 483 KQ -> NT (in Ref. 1).
 FT CONFLICT 599 599 D -> H (in Ref. 1).
 SQ SEQUENCE 1912 AA; 217628 MW; 996399DB4B074F21 CRC64;

Query Match 100.0%; Score 3446; DB 1; Length 1912;
 Best Local Similarity 100.0%; Pred. No. 4.8e-229;
 Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLKGRMDSEQSPSIGYSSRTLGPNGLILQALTLNADSGFNLERLEMLGDSFLKHAIT 60
 Db 1259 QVLKGRMDSEQSPSIGYSSRTLGPNGLILQALTLNADSGFNLERLEMLGDSFLKHAIT 1318
 Qy 61 TYLFCCTYPDAHEGRLSYMRKKVSNCLYRLGKKGLPSRMVVSIFDPPVNWLPPIGVVN 120
 Db 1319 TYLFCCTYPDAHEGRLSYMRKKVSNCLYRLGKKGLPSRMVVSIFDPPVNWLPPIGVVN 1378
 Qy 121 QDKSNTDKWEKDEMTKDCMLANGKLDDEYEEDEEEESLMWRAPKEEADYEDDFLEYDQE 180
 Db 1379 QDKSNTDKWEKDEMTKDCMLANGKLDDEYEEDEEEESLMWRAPKEEADYEDDFLEYDQE 1438
 Qy 181 HIRFIDNMLMGSGAFVKKISLSPFSTDSAYEWKMPKSSLGSMFSSDFEDFDYSSWDA 240
 Db 1439 HIRFIDNMLMGSGAFVKKISLSPFSTDSAYEWKMPKSSLGSMFSSDFEDFDYSSWDA 1498
 Qy 241 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDGTGKQISISYDLHTEQCIAADKSIADCEALLG 300
 Db 1499 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDGTGKQISISYDLHTEQCIAADKSIADCEALLG 1558
 Qy 301 CYLTSCGERAAQLFLCSLGLKVLPIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS 360
 Db 1559 CYLTSCGERAAQLFLCSLGLKVLPIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS 1618
 Qy 361 SRSSVLKDEYGLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFPKNAYLLQAFT 420

Db 1619 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAFT 1678
Qy 421 HASYHYNTITDCYQRLEFLGDAILDYLLITKHLYEDPRQHSPGVLTDLRSALVNMNTIFASL 480
Db 1679 HASYHYNTITDCYQRLEFLGDAILDYLLITKHLYEDPRQHSPGVLTDLRSALVNMNTIFASL 1738
Qy 481 AVKYDYHKYFKAVSPFLFHVDDFVQFQLEKNEMQGMDSSELRRSEDEEKEEDIEVPKAM 540
Db 1739 AVKYDYHKYFKAVSPFLFHVDDFVQFQLEKNEMQGMDSSELRRSEDEEKEEDIEVPKAM 1798
Qy 541 GDIFESLAGAIYMSGMSLETVMQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS 600
Db 1799 GDIFESLAGAIYMSGMSLETVMQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS 1858
Qy 601 PAERTYDGKVRVTVEVVGKGKFGVGRSRIAKSAAARRALRSLKANQPQVPNS 654
Db 1859 PAERTYDGKVRVTVEVVGKGKFGVGRSRIAKSAAARRALRSLKANQPQVPNS 1912

RESULT 2
A0MQH0_CRIGR
ID A0MQH0_CRIGR Unreviewed; 1917 AA.
AC A0MQH0;
DT 12-DEC-2006, integrated into UniProtKB/TrEMBL.
DT 12-DEC-2006, sequence version 1.
DT 24-JUL-2007, entry version 5.
DE DICER.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallerstorfer D.;
RL Submitted (SEP-2006) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; EF031271; ABK28790.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA:InterPro.
DR GO; GO:0004386; F:helicase activity; IEA:InterPro.
DR GO; GO:0004525; F:ribonuclease III activity; IEA:InterPro.
DR GO; GO:0006396; P:RNA processing; IEA:InterPro.
DR InterPro; IPR014001; DEAD-like_N.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001159; Ds_RNA_bd.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_III.
DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.